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(FILE 'HOME' ENTERED AT 10:55:02 ON 23 JUN 2003)

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 10:55:26 ON 23 JUN 2003

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 10:55:34 ON 23 JUN 2003

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     FILE 'CAPLUS, BIOSIS, SCISEARCH, MEDLINE, EMBASE, PASCAL, BIOTECHDS,
     CABA, LIFESCI, BIOTECHNO, TOXCENTER' ENTERED AT 10:56:49 ON 23 JUN 2003
L2           3068 S L1 AND (TRICHODERMA OR REESEI)
L3            993 S L2 AND (PURIF? OR CHARACT? OR CLON?)
L4              7 S L2 AND (BGL4 OR BGL4)
L5              1 DUP REM L4 (6 DUPLICATES REMOVED)
L6             15 S L1 AND BGL4
L7              3 DUP REM L6 (12 DUPLICATES REMOVED)
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L7 ANSWER 1 OF 3 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:597055 BIOSIS
DOCUMENT NUMBER: PREV200200597055
TITLE: Genomic studies of cell wall-associated synthases and hydrolases of Coccidioides immitis.
AUTHOR(S): Delgado, N. (1); Yu, J. J. (1); Hung, C. Y. (1); Nila, A. G. (1); Schaller, R. (1); Okeke, C. N. (1); Chen, X. (1); Cole, G. T. (1)
CORPORATE SOURCE: (1) Medical College of Ohio, Toledo, OH USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2002) Vol. 102, pp. 201. http://www.asmusa.org/mtgsrc/generalmeeting.htm. print. Meeting Info.: 102nd General Meeting of the American Society for Microbiology Salt Lake City, UT, USA May 19-23, 2002 American Society for Microbiology . ISSN: 1060-2011.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The fungal kingdom comprises a large group of uni- and multicellular eukaryotic organisms whose genomes range in size from 13-42 megabases (Mb). Coccidioides immitis (29 Mb genome) is characterized by a unique parasitic cycle in which inhaled arthroconidia grow isotropically and differentiate into large multinucleate spherules. The latter undergo segmentation and give rise to a multiplicity of endospores. These morphogenetic events involve major alterations in cell wall architecture. The C. immitis genome-sequencing project (more than 1X coverage at present) has revealed multiple families of genes which encode cell wall synthases and putative cell wall modifying enzymes (hydrolases). Representative genes include 4 glucan synthases (GLS), 6 chitin synthases (CHS), 7 **beta-glucosidases** (BGL), 3 beta-glucanosyltransferases (GEL), and 6 chitinases (CTS). We speculate that the coordinated regulation of expression of these enzymes is a requirement for appropriate development of parasitic cells. Macroarray hybridization studies have revealed upregulation of GLS3 (7.4-fold), BGL2 (3X), BGL5 (5X), BGL7 (3X), GEL1 (2.5X), and CTS1 (251X) in the endosporulation stage compared to the isotropic growth stage. Expression of the BGL1 gene is upregulated 3-fold in the segmentation stage compared to the isotropic growth stage. Expression of **BGL4**, CHS4, CHS5, and CHS6 show little variation throughout the parasitic phase. These families of C. immitis genes have extensively studied homologues in the Neurospora crassa (40 Mb) and Aspergillus fumigatus (30-35 Mb) genomes. On the other hand, C. immitis genes have been identified which show no homologues in the yeast or filamentous fungal genomes (e.g., genes which encode a spherule outer wall glycoprotein (SOWgp), and the Coccidioides-specific antigen (CSA)). Availability of the complete C. immitis genomic sequence will contribute to our understanding of the uniqueness of the parasitic cycle of this fungus, and help in the identification of potential molecular targets for development of novel antifungal drugs against coccidioidomycosis.

L7 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1
ACCESSION NUMBER: 1999:348867 CAPLUS
DOCUMENT NUMBER: 131:155115
TITLE: Molecular cloning and expression of the novel fungal **beta.-glucosidase** genes from Humicola grisea and Trichoderma reesei
AUTHOR(S): Takashima, Shou; Nakamura, Akira; Hidaka, Makoto; Masaki, Haruhiko; Uozumi, Takeshi
CORPORATE SOURCE: Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, 113-8657, Japan
SOURCE: Journal of Biochemistry (Tokyo) (1999), 125(4), 728-736

CODEN: JOBIAO; ISSN: 0021-924X
PUBLISHER: Japanese Biochemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A novel fungal .**beta**.-**glucosidase** gene (**bgl4**) and its homolog (bgl2) were cloned from the cellulolytic fungi Humicola grisea and Trichoderma reesei, resp. The deduced amino acid sequences of H. grisea **BGL4** and T. reesei BGL2 comprise 476 and 466 amino acids, resp., and share 73.1% identity. These .**beta**.-**glucosidases** show significant homol. to plant .**beta**.-**glucosidases** belonging to the .**beta**.-**glucosidase** A (BGA) family. Both genes were expressed in Aspergillus oryzae, and the recombinant .**beta**.-**glucosidases** were purified. Recombinant H. grisea **BGL4** is a thermostable enzyme compared with recombinant T. reesei BGL2. In addn. to .**beta**.-**glucosidase** activity, recombinant H. grisea **BGL4** showed a significant level of .beta.-galactosidase activity, while recombinant T. reesei BGL2 showed weak .beta.-galactosidase activity. Cellulose saccharification by Trichoderma cellulases was improved by the addn. of recombinant H. grisea **BGL4**.
REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 2
ACCESSION NUMBER: 1998:486295 CAPLUS
DOCUMENT NUMBER: 129:198717
TITLE: Identification, sequence analysis and expression studies of novel anther-specific genes of arabidopsis thaliana
AUTHOR(S): Rubinelli, Peter; Hu, Yi; Ma, Hong
CORPORATE SOURCE: Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 11724, USA
SOURCE: Plant Molecular Biology (1998), 37(4), 607-619
CODEN: PMBIDB; ISSN: 0167-4412
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Relatively little is known about pollen development at the mol. level. For the purpose of gaining understanding of the mol. control of pollen development, a no. of Arabidopsis cDNA fragments were isolated using subtractive hybridizations. DNA and RNA hybridizations and sequence analyses indicate that the authors have isolated cDNAs representing 13 genes. Sequences for 8 of these genes are novel, while those for the remaining 5 genes have substantial similarity to genes previously reported as anther- or pollen-specific. RNA in situ hybridizations with 5 genes revealed that four of them are tapetum-specific with differing temporal expression patterns during pollen development and one is pollen-specific within the flower. Sequence anal. of full-length cDNAs showed that one of the novel genes, ATA7, encodes a protein related to lipid transfer proteins. Another gene, ATA20, encodes a protein with novel repeat sequences and a glycine-rich domain that shares a predicted structure with a known cell wall protein. The full-length ATA27 cDNA encodes a protein similar to the **BGL4** .**beta**.-**glucosidase** from Brassica napus. The ATA27 protein is predicted to have an ER retention signal and an acidic isoelec. point, suggesting that it may be localized to the ER lumen. This may be a means of compartmentalization from its substrate(s). These studies demonstrate that subtractive hybridizations can be used to identify previously unknown genes, which should be valuable tools for further study of pollen and anther development and function.
REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2003 ACS DUPLICATE 1

ACCESSION NUMBER: 1999:348867 CAPLUS
DOCUMENT NUMBER: 131:155115
TITLE: Molecular cloning and expression of the novel fungal .**beta**.-**glucosidase** genes from Humicola grisea and **Trichoderma reesei**
AUTHOR(S): Takashima, Shou; Nakamura, Akira; Hidaka, Makoto; Masaki, Haruhiko; Uozumi, Takeshi
CORPORATE SOURCE: Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Tokyo, 113-8657, Japan
SOURCE: Journal of Biochemistry (Tokyo) (1999), 125(4), 728-736
CODEN: JOBIAO; ISSN: 0021-924X
PUBLISHER: Japanese Biochemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A novel fungal .**beta**.-**glucosidase** gene (**bgl4**) and its homolog (bgl2) were cloned from the cellulolytic fungi Humicola grisea and **Trichoderma reesei**, resp. The deduced amino acid sequences of H. grisea **BGL4** and T. **reesei** BGL2 comprise 476 and 466 amino acids, resp., and share 73.1% identity. These .**beta**.-**glucosidases** show significant homol. to plant .**beta**.-**glucosidases** belonging to the .**beta**.-**glucosidase** A (BGA) family. Both genes were expressed in Aspergillus oryzae, and the recombinant .**beta**.-**glucosidases** were purified. Recombinant H. grisea **BGL4** is a thermostable enzyme compared with recombinant T. **reesei** BGL2. In addn. to .**beta**.-**glucosidase** activity, recombinant H. grisea **BGL4** showed a significant level of .beta.-galactosidase activity, while recombinant T. **reesei** BGL2 showed weak .beta.-galactosidase activity. Cellulose saccharification by **Trichoderma** cellulases was improved by the addn. of recombinant H. grisea **BGL4**.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L3	L1 same bgl4	1	L3
DB=; PLUR=YES; OP=ADJ			
L2	L1 same bgl4	1	L2
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ			
L1	beta-glucosidase	1797	L1

END OF SEARCH HISTORY